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DATE: Wednesday, April 16, 2003

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT; PLUR=YES; OP=AND		
L1	relative same molecular same weight same electrophoresis same (variable or percent or variance or error or permissible)	40	L1
L2	relative same molecular same weight same electrophoresis same (variable$ or percent$ or varience$ or error$ or apparent$)	136	L2
L3	L2 not l1	97	L3
L4	L2 not l1	97	L4
L5	relative same actual same weight same (sds or page or sds-page or sdspage or electrophoresis)	29	L5
L6	(exact$ or calculated or calculate or actual$) same apparent same (kda or kd or dalton or daltons or kilodalton or kilodaltons or kilo-daltons or weight) same (sds or page or sds-page or sdspage or electrophoresis)	395	L6
L7	l6 same (variable$ or percent$ or varience$ or error$ or variation or assigned or assign)	51	L7
L8	L7 not l1 not l2 not l3 not l4 not l5	37	L8
L9	electrophoresis near10 accuracy	122	L9
L10	sds near10 percent	710	L10
L11	sds near10 differ$	2385	L11
L12	L11 same (kd or da or kda or k-da or kilodalton or daltons or dalton or kilo-dalton or mr or relative or weight)	774	L12
L13	5,733,976	1	L13

L3: Entry 4 of 97 File: USPT Mar 4, 2003

DOCUMENT-IDENTIFIER: US 6528098 B2
TITLE: Preparation of a therapeutic composition

Detailed Description Text (22):
The relative mass (Mr.): FIG. 5 shows the relative mass (measurement of molecular weight) of the two major peptide components of Product R resolved on a 16% SDS-Polyacrylamide gel electrophoresis (SDS-PAGE) and stained by silver stain using `SilverXpress` staining kit from NOVEX, following manufacturer-suggested protocol. Product R is resolved into two major silverstainable bands having apparent molecular weight of about 4.3 and about 5.2 KDa. A minor silver stainable component having molecular weight of about 7.6 KDa is also visible on an overloaded SDS-PAGE gel, and there may be trace amounts of other silverstainable peptides having molecular weights ranging from about 5 KDa to about 14 KDa. Coomassie Blue, a universal protein stain, stains the 4.3 KDa band extremely poorly. The three bands, 4.3 KDa, 5.2 KDa and 7.6 KDa, constitute more than about 90% of the peptides. Thus, Product R consists essentially of molecules having molecular weights below 8 KDa.

L3: Entry 50 of 97 File: USPT May 26, 1998

DOCUMENT-IDENTIFIER: US 5756334 A
** See image for Certificate of Correction **
TITLE: Thermostable DNA polymerase from 9.degree.N-7 and methods for producing the same

Detailed Description Text (15):
The apparent molecular weight of the DNA polymerase obtainable from T. litoralis is between about 90,000 to 95,000 daltons when compared with protein standards of known molecular weight, such as phosphorylase B assigned a molecular weight of 97,400 daltons. It should be understood, however, that as a protein from an extreme thermophile, T. litoralis DNA polymerase may electrophorese at an aberrant relative molecular weight due to failure to completely denature or other intrinsic properties. The exact molecular weight of the thermostable enzyme of the present invention may be determined from the coding sequence of the T. litoralis DNA polymerase gene. The molecular weight of the eluted product may be determined by any technique, for example, by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) using protein molecular weight markers.

L3: Entry 96 of 97 File: USPT Jun 15, 1982

DOCUMENT-IDENTIFIER: US 4335105 A
TITLE: Specific antigen vaccine for TGE in swine

Detailed Description Text (35):
For example, the procedure for obtaining an Rf value can be used as described by Bishop and Roy, J. Virol., 10, 234-243 (1972). In this procedure the polyacrylamide gel electrophoresis is carried out in the presence of sodium dodecyl sulfate (viz. 0.1% w/v) and urea (1.0 M). Using this procedure the SPA protein has an Rf value of 1.84.+-.0.01 (relative to human serum albumin). The other protein of Band B (which also has a buoyant density of 1.02 to 1.03 gm/ml) has a similarly determined Rf value of 1.40.+-.0.01. The presence of the sodium dodecyl sulfate assures determination of a charge-neutralized electrophoretic mobility (Rf value). The urea is used to cause the protein molecules to assume an "unwound" or more linear configuration thereby assisting the determination of an Rf value more nearly corresponding with true molecular weight. This procedure assumes, however, that the urea does not cause any alteration of protein size. The SPA protein as recovered by buoyant density separation is apparently decomplexed by the action of the urea. When polyacrylamide gel electrophoresis is carried out under the same conditions but in the absence of urea, the SPA protein has a charge-neutralized Rf value of 0.99.+-.0.01 (relative to bovine serum albumin). The molecular weight of the SPA protein calculated on the basis of its electrophoretic migration relative to that of bovine serum albumin (molecular weight=66,000) under these conditions is 67,000, which apparently, represents the SPA protein complex in its native state as it is released from the virion. The Rf value of 1.84.+-.0.01 determined in the presence of urea corresponds on the same basis to a calculated molecular weight of approximately 25,000.

huge difference

L3: Entry 94 of 97 File: USPT Jul 28, 1987

DOCUMENT-IDENTIFIER: US 4683135 A
TITLE: DSCG binding protein and process for preparing same

Brief Summary Text (28):
Surface radioiodinated RBL-2H3 cells (2.times.10.degree./ml) were incubated with a multivalent DSCG-BSA conjugate in a buffer solution for 1 hour at 4.degree. C. Unreacted DSCG-BSA was removed by several washings. Then, the cells were subjected to solubilization with a non-ionic detergent (1% NP-40). Nonspecific, clearing precipation was obtained by reacting one ml of the lysate with goat antilysozyme serum and lysozyme. Lysates were allowed to precipitate for 24 hours and later spun down at 13,000 g and the pellets discarded. The DSCG binding protein was subsequently precipitaed from those lysates with rabbit anti-DSCG antibodies and DSCG-BSA as a carrier. The immune precipitate formed was spun down and washed with PBS containing 0.1% NP-40. The washed precipitates were dissolved in SDS sample buffer and subjected to polyacrylamide gel electrophoresis. Only a single readioactive band, of 60,000 molecular weight, was observed (FIG. 1). The meracaptoethanol-reduced precipitate also yielded one band on PAGE, yet it was retarded relative to the unreduced protein, hence having an apparent molecular weight of 75,000 (FIG. 1).

L3: Entry 90 of 97 File: USPT Jan 8, 1991

DOCUMENT-IDENTIFIER: US 4983521 A
TITLE: Transmembrane integrator sequences

Detailed Description Text (95):
Upon expression in a transcription-coupled rabbit reticulocyte lysate cell-free translation system, pSPGP1 encoded a fusion protein of -32 kD with both globin and prolactin immunoreactivity called preGSP. When translation reactions were supplemented with microsomal membranes two additional translation products, not present in the absence of membranes, were seen after electrophoresis on polyacrylamide gels in SDS with subsequent autoradiography. One of these bands, termed P1, was found to be anti-prolactin but not anti-globin immunoreactive and to co-migrate with authentic mature bovine prolactin. The other product, termed GS1, was anti-globin but not anti-prolactin immunoreactive, and migrated with an apparent molecular weight slightly greater than that of authentic full-length globin. When membranes were added after completion of protein synthesis with further incubation, neither of these bands were generated. The difference in the relative intensities of the bands in the autoradiographs is due to the methionine distribution in the [.sup.35 S]methionine-labeled, newly synthesized proteins. Upon processing, of the eleven methionines in preGSP, P1 contains seven and GS1 only four.

L5: Entry 12 of 29 File: USPT Dec 12, 1995

DOCUMENT-IDENTIFIER: US 5474700 A
TITLE: Industrial alkaline protease from shipworm bacterium

Detailed Description Text (6):
While not desiring to be bound by any particular theory, there is a plausible explanation for the large discrepancy in the molecular mass values obtained by the various methods. The low mass (17,600 daltons) obtained by gel permeation HPLC may have resulted from nonspecific interaction of the protein with the column resin, retarding its elution. However, varying the ionic strength of the eluent, addition of detergent or addition of exogenous protein did not significantly alter the elution profile of the protease. A molecular mass of 17,600 is also in good agreement with the nominal molecular weight cutoff values of the ultrafiltration membranes used in the purification scheme described in Example 2. The molecular mass of 36,000 daltons determined by SDS-PAGE and the mass of 46,000 daltons determined by zonal density-gradient centrifugation suggests that the native protease is a dense, tightly folded molecule. For such an enzyme, sedimentation behavior, which is strongly and directly dependent on protein density, would be expected to yield an anomalously high apparent molecular mass relative to standard proteins. Conversely, estimates of molecular mass by HPLC and those suggested by ultrafiltration behavior would be anomalously low, as both determinations depend primarily on the radii of molecules. A denser, more tightly folded molecule should possess a smaller radius in comparison to equivalent molecular mass standards. The molecular mass determined by SDS-PAGE should be close to the actual molecular mass of the protease. Other characteristics of the protease are described in further detail in Example 3.

L12: Entry 709 of 774 File: USPT Jan 30, 1990

DOCUMENT-IDENTIFIER: US 4897354 A
** See image for Certificate of Correction **
TITLE: Monoclonal antibody-specific merozoite antigens

Brief Summary Text (6):
Workers studying the merozoite in P. falciparum have reported a class of polypeptides in merozoites (and their schizont precursors) with molecular weights varying over the range of 185,000 to 200,000 (185K to 200K). The variation in reported molecular weights is in part a reflection of the fact that relative molecular weight (M.sub.r) estimates using SDS-PAGE are approximations, but the variation is also attributable to real differences in the polypeptides isolated from different malaria isolates. Molecules within this class of polypeptides have been referred to at various times, inter alia, as pf195, P195, P190, gp185, P200 and polymorphic schizont antigens (PSA). Polypeptides within this class have been reported on occasion to be surface molecules, to be antigenic in nature, and to be precursors for surface fragments of smaller molecular weight.

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L8: Entry 4 of 37 File: USPT May 21, 2002

DOCUMENT-IDENTIFIER: US 6391557 B1
TITLE: Nucleic acid molecule encoding a mismatch endonuclease and methods of use thereof

Detailed Description Text (95):
The amino acid sequence of the N-terminal and three other internal proteolytic peptides of CEL I, identified by Edman degradation performed by the Protein/DNA Technology Center of the Rockefeller University, are shown in FIG. 2 in bold letters. The 72 amino acids identified represent about 28% of the CEL I polypeptide and were completely accounted for in the cDNA sequence. CEL I without the leader sequence is a protein of 274 amino acid residues, with a calculated molecular weight of 31,440.2. Compared with the apparent molecular weight of 43 KDa determined in SDS PAGE, CEL I is 27 percent carbohydrate by weight.

L8: Entry 6 of 37 File: USPT Jul 24, 2001

DOCUMENT-IDENTIFIER: US 6265214 B1
TITLE: Methods and compositions for inducing monocyte cytotoxicity

Brief Summary Text (16):
When subjected to gel filtration chromatography, the factor has an apparent molecular weight of approximately 11,500 Daltons when chromatographed under the conditions described herein. Again, as with gel electrophoresis, it will be appreciated that gel filtration chromatography does not provide an exact molecular weight determination, rather such molecular weight determinations appear as a broad elution of monocyte cytotoxicity inducing activity, wherein the peak activity elutes from such columns at a position which corresponds to approximately 11,500 Daltons. However, this molecular weight may vary with variations in conditions, for example, running buffer, exclusion limit, column size and the particular gel filtration methodology which is utilized.

L8: Entry 10 of 37 File: USPT Jan 4, 2000

DOCUMENT-IDENTIFIER: US 6010999 A
TITLE: Stabilization of fibroblast growth factors by modification of cysteine residues

Detailed Description Text (149):
Molecular weight determinations are performed on a 10 to 15% gradient and 20% homogeneous polyacrylamide gels in the presence of sodium dodecyl sulfate (SDS-PAGE) using a silver stain detection system (Phastgel System, Pharmacia/LKB). hbFGF (2-155) migrates with an M.sub.r of 17,000 compared to an M.sub.r value of about 19,000 for glu.sup.3,5 hbFGF. Molecular weights calculated from amino acid sequence data for hbFGF and the chimeric version are 17,124 and 17,224, respectively. To resolve the apparent molecular weight discrepancy, a sample of glu.sup.3,5 hbFGF is analyzed by liquid-secondary ion mass spectrometry and gives a molecular ion of mass 17,365. This value is, within experimental error, consistent with that predicted from sequence data. While not wishing to be bound to any theory, the anomalous migration of glu.sup.3,5 on polyacrylamide gels under denaturing conditions is most likely due to interference of protein-SDS interactions from the glutamyl side chains at positions 3 and 5.

L8: Entry 13 of 37 File: USPT Mar 16, 1999

DOCUMENT-IDENTIFIER: US 5882876 A
TITLE: Malignant cell type markers of the interior nuclear matrix

Detailed Description Text (83):
The primary structure of MT1, represented in FIG. 1, contains 27 proline residues which generally occur in pairs or triplets throughout the molecule. The proline distribution within the sequence is illustrated in FIG. 1A, where diamonds represent the proline residues. Proline pairs and triplets are indicted by stacked diamonds. At the N terminus, a 40 amino acid stretch contains a cluster of 8 prolines (residues 42-81, Seq. ID No. 1) that occur as pairs separated by 3 or fewer amino acids. A similar proline-rich region occurs in the C terminus of MT1 (residues 551-563) where 6 prolines occur in a 13 amino acid stretch. Both proline-rich regions likely lie on the protein surface, based on probability calculations determined by the technique of Emini et al. (1985) J. Virol. 55:836-839. The high proline density also may explain the anomalous apparent molecular weight of the protein as determined by SDS polyacrylamide gel electrophoresis. As described above, the predicted molecular weight for MT1, calculated from the amino acid sequence, is 70.1 kD. However, as described below, both the natural-sourced and recombinant protein migrate as a 90 kD protein on an SDS polyacrylamide gel. Alternatively, it is also possible that the molecular weight variation may result from some post-translational modification achievable in both prokaryotic and eukaryotic cells.

L8: Entry 19 of 37 File: USPT Jul 18, 1995

DOCUMENT-IDENTIFIER: US 5434247 A
TITLE: Peptides for inducing monocyte cytotoxicity in diagnostics

Brief Summary Text (18):
The smaller polypeptide of MCF (P14.7) has an apparent molecular weight of approximately 11,500 Daltons when subjected to gel filtration chromatography under the conditions described herein. Again, as with gel electrophoresis, it will be appreciated that gel filtration chromatography does not provide an exact molecular weight determination. In this case, the monocyte cytotoxicity inducing activity elutes from such columns as a broad peak, corresponding to a molecular weight of approximately 11,500 Daltons. However, this molecular weight may vary with variations in conditions, for example, running buffer, exclusion limit, column size and the particular gel filtration methodology which is utilized.

L8: Entry 20 of 37 File: USPT Jul 4, 1995

DOCUMENT-IDENTIFIER: US 5430129 A
TITLE: Purified, native dystrophin

Detailed Description Text (35):
Alkaline treatment followed by a 3 h sucrose gradient centrifugation time (FIG. 3A) completely separated dystrophin from the 50 kDa, 43 kDa, 35 kDa and 25 kDa glycoprotein multiplet of the dystrophin-glycoprotein complex. However, this procedure was not sufficient to purify dystrophin from the high M.sub.r glycoproteins which contaminate dystrophin-glycoprotein complex preparations and cosediment with uncomplexed dystrophin (FIG. 3B). In order to completely purify dystrophin, the high M.sub.r glycoproteins which contaminated peak dystrophin-containing gradient fractions (FIG. 3B) were removed by WGA-sepharose adsorption (FIG. 4). Ninety-eight percent of the protein in the WGA void appeared as a single high M.sub.r band on overloaded Coomassie Blue-stained gels while the remaining 2% of protein composed a band of slightly lower M.sub.r (FIG. 4). Although it is difficult to accurately determine the M.sub.r of extremely large proteins by SDS-PAGE the predominant band in six consecutive preparations was calculated to have an average apparent M.sub.r of 400.+-.6 kDa which is in close agreement with the predicted M.sub.r. The predominant component appears to be intact dystrophin as it is recognized by antisera specific for either the amino-or carboxyl-terminals of human skeletal muscle dystrophin (FIG. 5). The minor, lower M.sub.r component in the dystrophin preparation was stained only by the carboxyl-terminal specific antisera (FIG. 5) indicating that it is most likely a proteolytic fragment. Also shown in FIG. 5, the affinity-purified carboxyl-terminal antisera does not recognize the synthetic peptide corresponding to the carboxyl-terminal of the chromosome 6 dystrophin-related protein. Nitrocellulose transfers stained with peroxidase-conjugated WGA revealed no contaminating glycoproteins in the pure dystrophin (FIG. 4). The average yield of pure dystrophin was 30 micrograms when 1.2-1.5 of rabbit skeletal muscle membranes was used as starting material.

L8: Entry 29 of 37 File: USPT Dec 11, 1990

DOCUMENT-IDENTIFIER: US 4977245 A
TITLE: Methods and compositions for inducing monocyte cytotoxicity

Brief Summary Text (15):
The present invention is directed to a composition which includes substantially purified human mondyte cytotoxicity inducing factor, also referred to herein as MCF. The composition includes a substantially purified soluble factor capable of inducing human monocytes to a cytotoxic state, the factor having a molecular weight of between about 18,100 and about 14,700 Daltons when determined by polyacrylamide gel electrophoresis under the conditions as described herein. It will be appreciated that under differing electrophoresis conditions, this molecular weight may vary. When subjected to gel filtration chromatography, the factor has an apparent molecular weight of approximately 11,500 Daltons when chromatographed under the conditions described herein. Again, as with gel electrophoresis, it will be appreciated that gel filtration chromatography does not provide an exact molecular weight determination, rather such molecular weight determinations appear as a broad elution of monocyte cytotoxicity inducing activity, wherein the peak activity elutes from such columns at a position which corresponds to approximately 11,500 Daltons. However, this molecular weight may vary with variations in conditions, for example, running buffer, exclusion limit, column size and the particular gel filtration methodology which is utilized.

L8: Entry 31 of 37 File: USPT Dec 30, 1986

DOCUMENT-IDENTIFIER: US 4632780 A
TITLE: N-terminal fragment of human pro-opiomelanocortin and process therefor

Detailed Description Text (55):
Said last-named material was further purified by HPLC on a semi-preparative column (0.70.times.25 cm) of Beckman.RTM. 5-Micron Ultrasphere ODS.RTM. using 0.02M triethylammonium formate (TEAF) pH 3.0 as the aqueous buffer and 2-propanol as the organic eluant. A linear gradient starting from 20% 2-propanol:80% TEAF up to 47% 2-propanol:53% TEAF was used at a flow rate of 2 ml/min and a duration of 90 min. The HPLC apparatus used was a Waters liquid chromatograph Model 204 equipped with a waters Model 450 U.V. detector, monitoring absorption at 280 nm. Each peak was collected, lyophylized, and a weighed portion was subjected to quantitative radio-immunoassay using a porcine N-terminal antibody recognizing the gamma-MSH sequence, see FIG. 1A. Based on a standard displacement curve the amount of human N-terminal fragment in each fraction was calculated as a percentage by weight. The peaks denoted V+VI were then repurified under the same conditions and gave the substantially pure N-terminal fragment of human pro-opiomelanocortin, viz., the glycopeptide of formula I, as a colourless, fluffy solid (15 mg). The glycopeptide of formula I is characterized by having a peak of absorption at 280 nm eluted at 32-34 percent 2-propanol and 68-66 percent 0.02M TEAF when subjected to HPLC on a Waters.RTM. Micro-Bondapak C-18.RTM. column with a gradient of 20 percent to 60 percent 2-propanol over 80 minutes at a flow rate of 1 ml/min., see FIG. 1B. The glycopeptide is further characterized by its amino acid analysis shown in Table 1, by its chemical structure shown in formula I, and by an apparent molecular weight of 16000-18000 as determined by SDS-polyacrylamide gel electrophoresis.

L9: Entry 101 of 122 File: USPT Aug 4, 1992

DOCUMENT-IDENTIFIER: US 5135870 A
TITLE: Laser ablation/ionizaton and mass spectrometric analysis of massive polymers

Brief Summary Text (5):
Heretofore, the best known method for the determination of protein and nucleic acid masses is gel electrophoresis which at best has an accuracy of .+-.5%. Presently, the only method known for determining polymer size distribution is a gel permeation method which is recognized as imprecise and only measures relative sizes. More accurate mass spectrometric methods have been reported recently for protein mass determination, but this approach has not been extended to other polymers.

L12: Entry 2 of 774 File: USPT Apr 1, 2003

DOCUMENT-IDENTIFIER: US 6541616 B1
TITLE: Moraxella catarrhalis protein, gene sequence and uses thereof

Detailed Description Text (10):
According to various aspects of the invention, the polypeptides of the invention are characterized by their apparent molecular weights based on the polypeptides' migration in SDS-PAGE relative to the migration of known molecular weight markers. While any molecular weight standards known in the art may be used with the SDS-PAGE, preferred molecular weight markers comprise carbonic anhydrase, trypsin inhibitor and lysozyme. One skilled in the art will appreciate that the polypeptides of the invention may migrate differently in different types of gel systems (e.g., different buffers; different types and concentrations of gel, crosslinker or SDS). One skilled in the art will also appreciate that the polypeptides may have different apparent molecular weights due to different molecular weight markers used with the SDS-PAGE. Hence, the molecular weight characterization of the polypeptides of the invention is intended to be directed to cover the same polypeptides on any SDS-PAGE systems and with any molecular weight markers which might indicate sightly different apparent molecular weights for the polypeptides than those disclosed here.

L12: Entry 6 of 774 File: USPT Mar 11, 2003

DOCUMENT-IDENTIFIER: US 6531305 B1
TITLE: Sperm associated protein kinase polypeptides, corresponding nucleic acids, and methods of use

Detailed Description Text (149):
The MALDI TOF mass spectra for C.sub.s had a single peak corresponding to a mass of .about.39.9 kDa, whereas those for C.sub.sm had a single peak of .about.40.8 kDa. The spectrum for an equimolar mixture of C.sub.s and C.sub.sm, revealed two well separated peaks with masses of 39,832 Da and 40,722 Da. Although some error is to be expected for the estimated masses of proteins of this size, the mass difference obtained by comparing two proteins in the same spectrum is quite accurate. Therefore, C.sub.s is .about.890 Da smaller than C.sub.sm, confirming the apparent difference in mass observed by SDS-PAGE. The results also confirm the purity of the C.sub.s and C.sub.sm preparations. The observed mass for ovine C.sub.sm was reasonably close to that predicted for bovine somatic C.alpha.1 with a myristylated glycine at the amino-terminus (40,858 Da).

L12: Entry 13 of 774 File: USPT Feb 11, 2003

DOCUMENT-IDENTIFIER: US 6517828 B1
TITLE: C-CAM as an angiogenesis inhibitor

Detailed Description Text (57):
It is known that the migration of a polypeptide can vary, sometimes significantly, with different conditions of SDS/PAGE (Capaldi et al., 1977). It will therefore be appreciated that under differing electrophoresis conditions, the apparent molecular weights of purified or partially purified expression products may vary. Angiostatin is a protein having a molecular weight of between approximately 38 kilodaltons and 45 kilodaltons as determined by reducing polyacrylamide gel electrophoresis (U.S. Pat. No. 5,733,876, specifically incorporated herein by reference).

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L12: Entry 19 of 774 File: USPT Jan 14, 2003

DOCUMENT-IDENTIFIER: US 6506384 B1
TITLE: Early detection of mycobacterial disease

Detailed Description Text (243):
Evaluations of the effects of O-glycosylation on the conformation of proteins indicate that the presence of sugar units in heavily clustered domains limits protein folding, leading to extended conformations of the protein in these areas. Thus, in the context of MPT 32, it is probable that the combination of glycosyl units in the vicinity of a preponderance of Pro residues will ensure a minimum of secondary or tertiary structure leading to a "stiff," extended conformation. This feature explains the dramatic difference in the predicted molecular mass of 45 kDa based on mobility in SDS-PAGE compared to the true molecular weight of 30.2 kDa (Laqueyrerie, A. et al., supra).

L12: Entry 38 of 774 File: USPT Oct 1, 2002

DOCUMENT-IDENTIFIER: US 6458532 B1
TITLE: Polynucleotides encoding IMP.18p myo-inositol monophosphatase and methods of detecting said polynucleotides

Detailed Description Text (42):
As used herein, "calculated molecular weight" of a polypeptide or peptide is the molecular weight based on the polypeptide's or peptide's deduced amino acid sequence--the deduced translation product--as encoded by the corresponding nucleic acid. In contrast, the "apparent" molecular weight is measured, empirical value. The apparent molecular weight of a protein can be determined by many different methods, all known to one of skill in the art. Some methods of determination include: SDS gel electrophoresis, native gel electrophoresis, molecular exclusion chromatography, zonal centrifugation, mass spectroscopy. Disparity between results of different techniques can be due to factors inherent in the technique. For example, native gel electrophoresis, molecular exclusion chromatography and zonal centrifugation depend on the size of the protein. The proteins that are cysteine rich can form many disulfide bonds, both intra- and intermolecular. SDS gel electrophoresis depends on the binding of SDS to amino acids present in the protein. Some amino acids bind SDS more tightly than others, therefore, proteins will migrate differently depending on their amino acid composition. Mass spectroscopy and calculated molecular weight from the sequence in part depend upon the frequency that particular amino acids are present in the protein and the molecular weight of the particular amino acid. If a protein is glycosylated, mass spectroscopy results will reflect the glycosylation but a calculated molecular weight may not.